

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 06:22:02 : Search time 10069.4 Seconds
(without alignments)
3254.293 Million cell updates/sec

Title: US-09-227-881-1
Perfect score: 5300
Sequence: 1 atcttgctcagttacctc.....cagcaccctctcagcacagc 5300

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 segs, 3091403243 residues
Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *
12: gb_est12: *
13: gb_est13: *
14: gb_est14: *
15: gb_est15: *
16: gb_est16: *
17: gb_est17: *
18: gb_est18: *
19: gb_est19: *
20: gb_est20: *
21: gb_est21: *
22: gb_est22: *
23: gb_est23: *
24: gb_est24: *
25: gb_est25: *
26: gb_est26: *
27: gb_est27: *
28: gb_est28: *
29: gb_est29: *
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34: gb_est34: *
35: gb_est35: *
36: gb_est36: *
37: gb_est37: *
38: gb_est38: *
39: gb_est39: *
40: gb_est40: *
41: em_est4a: *
42: em_estfun: *
43: em_esthum1: *

44: em_esthum2: *
45: em_esthum3: *
46: em_esthum4: *
47: em_esthum5: *
48: em_esthum6: *
49: em_esthum7: *
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52: em_esthum10: *
53: em_esthum11: *
54: em_esthum12: *
55: em_esthum13: *
56: em_esthum14: *
57: em_esthum15: *
58: em_esthum16: *
59: em_esthum17: *
60: em_esthum18: *
61: em_esthum19: *
62: em_esthum20: *
63: em_estin1: *
64: em_estin2: *
65: em_estin3: *
66: em_estin4: *
67: em_estom: *
68: em_estov1: *
69: em_estov2: *
70: em_estp1: *
71: em_estp12: *
72: em_estp13: *
73: em_estp14: *
74: em_estp15: *
75: em_estro1: *
76: em_estro2: *
77: em_estro3: *
78: em_estro4: *
79: em_estro5: *
80: em_estro6: *
81: em_estro7: *
82: em_estro8: *
83: em_estro9: *
84: em_estro10: *
85: em_estro11: *
86: em_estro12: *
87: em_estro13: *
88: gb_gss1: *
89: gb_gss2: *
90: gb_gss3: *
91: gb_gss4: *
92: em_gss1: *
93: em_gss2: *
94: em_gss3: *
95: em_gss4: *
96: gb_gss5: *
97: gb_gss6: *
98: gb_gss7: *
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103: gb_gss12: *
104: gb_gss13: *
105: gb_gss14: *
106: gb_gss15: *
107: gb_gss16: *
108: gb_gss17: *
109: gb_gss18: *
110: gb_gss19: *
111: gb_gss20: *
112: gb_gss21: *
113: gb_gss22: *
114: gb_gss23: *
115: gb_gss24: *
116: em_gss5: *

117: em_gss6:*
118: em_gss7:*
119: em_gss8:*
120: em_gss9:*
121: em_gss10:*
122: em_gss11:*
123: em_gss12:*
124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	180.8	3.4	660	88	A0057239	CIT-HSP-2
2	179.8	3.4	539	96	A0379787	AQ379787 RPT11-15
3	179	3.4	645	100	A0636457	A0636457 RPT1-14
4	178.4	3.4	678	96	AQ387027	AQ387027 RPT11-15
5	177.6	3.4	537	25	AW978041	AW978041 EST390150
6	177.4	3.3	516	89	AQ112451	AQ112451 CIT-HSP-2
7	177.2	3.3	577	91	AQ265389	AQ265389 CITBI-E1
8	176.6	3.3	548	11	A1583291	A1583291 tC56902.x
9	176.6	3.3	434	90	AQ199435	AQ199435 RPT11-58
10	176.6	3.3	591	25	AW979191	AW979191 EST391301
11	176	3.3	521	21	AW273360	AW273360 x138a04.x
12	176	3.3	551	39	T53829	T53829 yB5610.01
13	175.8	3.3	589	91	AQ283440	AQ283440 RPT11-79
14	175.4	3.3	386	98	AQ474222	AQ474222 CITBI-E1
15	175.2	3.3	711	97	AQ415030	AQ415030 RPT1-11-2
16	175	3.3	388	19	AW069227	AW069227 C141h09.x
17	175	3.3	421	23	AW674631	AW674631 b41a11.x
18	175	3.3	447	24	AW820784	AW820784 RC2-ST030
19	175	3.3	454	12	A1634187	A1634187 t555a08.x
20	175	3.3	474	10	A157313	A157313 l173a05.x
21	175	3.3	527	11	A1523813	A1523813 t996d09.x
22	174.8	3.3	432	9	A1300818	A1300818 g47c06.x
23	174.8	3.3	435	9	A1300818	A1300818 g47c06.x
24	174.6	3.3	424	10	A1431513	A1431513 t45f04.x
25	174.6	3.3	677	110	B66612	B66612 CIT-HSP-201
26	174.2	3.3	342	6	AA846923	AA846923 ge06d01.s
27	173.8	3.3	460	110	B15692	B15692 345N8-TP-C1
28	173.8	3.3	565	25	AW953220	AW953220 EST365290
29	173.6	3.3	368	21	AW270385	AW270385 xp74f06.x
30	173.6	3.3	374	37	F35684	F35684 HSPD32531.H
31	173.4	3.3	384	7	AA682029	AA682029 c146e04.s
32	173.4	3.3	427	5	AA550989	AA550989 nj36d12.s
33	173.4	3.3	436	88	AQ021084	AQ021084 CIT-HSP-2
34	173.4	3.3	486	8	A1049955	A1049955 an38e01.x
35	173.4	3.3	642	110	B59854	B59854 CIT-HSP-345
36	173.4	3.3	836	102	AQ071745	AQ071745 HS-3122.A
37	173.2	3.3	413	102	A1355246	A1355246 q474b06.x
38	173.2	3.3	430	13	A1859906	A1859906 w423c01.x
39	173.2	3.3	508	100	AQ632598	AQ632598 RPT1-11-4
40	173.2	3.3	784	101	AQ738890	AQ738890 HS-5382.B
41	172.8	3.3	496	4	AA486819	AA486819 ab19c10.x
42	172.8	3.3	624	96	AQ373399	AQ373399 RPT11-15
43	172.6	3.3	300	7	AA937809	AA937809 nw89b02.s
44	172.4	3.3	397	10	A1417469	A1417469 th33h09.x
45	172.4	3.3	439	14	A1961983	A1961983 wt41a12.x

ALIGNMENTS

RESULT 1
A0057239

LOCUS A0057239 660 bp DNA GSS 30-JUL-1998
DEFINITION CIT-HSP-2340D14.TF CIT-HSP Homo sapiens genomic clone 2340D14, DNA
SEQUENCE
ACCESSION A0057239
VERSION A0057239.1 GI:3353765
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 660)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Sun,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
TITLE Unpublished (1998)
JOURNAL Other_GSSs: CIT-HSP-2340D14.TF
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source 1..660
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2340D14"
/clone_1fb="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"
BASE COUNT 116 a 188 c 150 g 206 t
ORIGIN
Query Match 3.4%; Score 180.8; DB 88; Length 660;
Best Local Similarity 86.0%; Pred. No. 8e-22;
Matches 215; Conservative 0; Mismatches 27; Indels 8; Gaps 1;
QY 1321 accgagctcactgcaacctctgctcccaagttcaagcaattctctctcagctctc 1380
|||||
DB 293 ATCTGACGTCACCTGCAACCTGCTCCCGGGTCAAGCATTCCTGTCACACCTCC 352
QY 1381 cgcgcagctcgggactcaggcg-----cagcccggtcatttttgtattgtacta 1432
|||||
DB 333 CAAATGACGTCGATTACAGGCGCACACACACCGCCGCGTAATTTTGTATTACTA 412
QY 1433 gggatggggtttccaccattatggccgctgctgttgaacctctgacctcaggtatcca 1492
|||||
DB 413 GAGATGGGGTTTACACCATGTTGGCCAGGCTGCTCGAATCTCTACCTCAGATATCA 472
QY 1493 ccacactcagctccttaagtgtcgtggaattcaagcatgagttcacccgcccgaagg 1552
|||||
DB 473 CCCACTGCTGCTCCCAAGATGCTGGATTTACAGGCTTGCGGCACTGGCCAGCCTAAT 532
QY 1553 gtcaagtctt 1562
|||||
DB 533 TTTTGTATT 542
RESULT 2
AQ379787 539 bp DNA GSS 20-MAY-1999
LOCUS AQ379787
DEFINITION RPT11-152C3.TF RPT1-11 Homo sapiens genomic clone RPT1-11-152C3,

ACCESSION	DNA sequence.
VERSION	A0379787
KEYWORDS	A0379787.1 GI:4350810
SOURCE	GSS.
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 539)
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter, J.C.
TITLE	USE OF BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL	Unpublished (1997)
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pietere@jng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (intel@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..539 /organism="Homo sapiens" /db_xref="GDB:7558034" /db_xref="taxon:9606" /clone="RPCI-11-152C3" /clone_id="RPCI-11" /sex="Male" /cell-type="Lymphocytes" /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT	187 a 112 c 123 g 116 t 1 others
ORIGIN	
Query Match	3.4%; Score 179.8; DB 96; Length 539;
Best Local Similarity	76.8%; Pred. No. 1.2e-21;
Matches 235; Conservative	0; Mismatches 63; Indels 8; Gaps 1
Oy	1280 aggggagagggtcttgcttacaccactgatgtctcaccactgaagtcaactgaacc 1339
Db	327 AGAGTCTGGCTTGTCACACGAGCTGGAGTTCAGTGGCGGATCTGGGTCACTGCAACC 268
Oy	1340 tcctgcctcccaagttcaagaacaattccctgcttcacagccctcccgctagcttggaactaac 1399
Db	267 TCTGCCTCCCGGGTTCACAACAAATTCTCGCTCACACCTCCGAGTAGCTGGAGCACAG 208
Oy	1400 gc-----gcagcccgcgctaatttttgtatgttagtaagaatggggtttcacata 1451
Db	207 GCATGTGCCACCATACCCCGCTAATTTTTGTATTTTATAGAAAGGGGTTTCACACATG 148
Oy	1452 tttagccggcgtgctcttgacctcctgaacteaagtgatcacaccacctcagctcttaa 1511
Db	147 TTGGCCAGGCTGTCTTGAACTCTGACTCAGGTATCACCAGGCTTGCCCTCTAA 88
Oy	1512 gtctctggaattcaagcatgaatcaaccgcccgcccaaaggltcagtgittataaagaa 1571
Db	87 GGCTGGGATTCACAGACGAGATCACACGCGCGCTCAAAATCCCTTTTACAGCTTA 28
Oy	1572 taactt 1577
Db	27 TGAATT 22

RESULT	3
A0636457/c	GSS
LOCUS	17-JUN-1999
DEFINITION	RPC11-11-465121.tJ RPC1-11 Homo sapiens genomic clone RPC1-11-465121 DNA sequence.
ACCESSION	A0636457
VERSION	A0636457.1 GI:5099092
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 645)
AUTHORS	Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter J.C.
TITLE	Use of BAC End Sequences from Library RPC1-11 for Sequence-Ready Map Building
JOURNAL	Unpublished (1997) Contact: Shaying Zhao, William Niernan, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301 838 0200 Fax: 301 838 0208
COMMENT	Email: hbe@tigr.org Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pietere@jorg.med.buffalo.edu). Clones may be purchased from BACPac Resources (http://bacpac.med.buffalo.edu/ordering/) or from Research Genet cs (inforesgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: SP6 Class: LOC ends. Location/Qualifiers
FEATURES	Source
source	1..645 /organism="Homo sapiens" /db_xref="GDB:7678388" /dn_xref="taxon:9606" /cloned="RPC1-11-465121" /clone_id="RPC1-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human male BAC library"
BASE COUNT	214 a 118 c 139 g 174 t
ORIGIN	
Query Match	3.4% Score 179; DB 100; Length 645;
Best Local Similarity	88.2%; Pred. No. 1.7e-21;
Matches 209; Conservative	0; Mismatches 20; Indels 8; Gaps 1;
OY	1322 ctggagctcaactgcaacctgcgtccaccagtccaagaattcctcttcgaagctccc 1381
Dd	248 CTTCAGCTCAGTGCACACTGTGGCCCGAAGTTCAAGTAATTCCTGCCACAGCTCCC 189
OY	1382 gcgttagctcyggaactacaaggcg-----cacgccgcgcctaatttgatgtagtag 1433
Dd	188 GAGTAGTGAGATTACAGCGCGTGCTCACACAGCCACCAGCTAAATTTTGTATTTTAGTAG 129
OY	1434 agatgtgggttttaacatattagaccgcgctgttgtcgaactcctgaaccctcagtgatccaac 1493
Dd	128 AGATGGGAATTCACCATGTGGCCAGCGCTGGTCTCCGACTCCTGACCTCAAGTAGTATTC 69
OY	1494 ccacctcagcctccccaaagtctgtgagattcaaggcataagctcagcgcccgcccaa 1550
Dd	68 CCACCTCAGCTCCCCAAAGTGTGGGATTACAGGCATAGCCACCGCCGCCCAA 12
RESULT	4
A0387027/c	GSS
LOCUS	21-MAY-1999
DEFINITION	RPc11-1153C12.TJ RPc1-11 Homo sapiens genomic clone RPc1-11-153C12, 678 bp DNA

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 516)
AUTHORS	Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Lanher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wilde, C., Shizuya, H., Simon, M. and Venter, J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other_GSSs: CIT-HSP-2372C9.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdamas@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..516 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2372C9" /clone_1lb="CIT-HSP" /sex="Male" /cell_type="Sperm" /note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	
Query Match	3.4%; Score 177.6; DB 89; Length 516;
Best Local Similarity	85.2%; Pred. No. 3e-21;
Matches 213: Conservative	0; Mismatches 29; Indels 8; Gaps 1
Oy	1321 accctgagctcactgtcaacctctgctcccaaggttcaagaatctctgltctcagctcc 1380
Db	255 ATCTACAGCTCACTGCACACTGTGCTCCGGGTTCAAGGATTCCTCTCAAGCTCC 314
Oy	1381 cgcgtagctggaactaagcg-----caagcccggttaattttgtatgttaagta 1432
Db	315 CAAGTAGCTGGGATTAACAGCGCACACACACACGCGGCTTAATTTTGTATTTTAACTA 374
Oy	1433 gagatggaggttcacacattagcccgcggtgtgtcttgaactctctgacctcaggtgtaca 1492
Db	375 GAGATGGGGTTTCACCATTTTGGCCAGCGCTGTGCTCGAATCTCTGACTTAAGTGTATCCA 434
Oy	1493 ccacctcagacctctcaagtgctggatattacaggaattagatcaccgcgcgcgccaag 1552
Db	435 CCCACCTTGCTCCCAAGGTGTGGATTAACAGGCTTGCGCACTGGCCCAAGCTTAAT 494
Oy	1553 gtcaagtgttt 1562
Db	495 TTTTGCATTT 504
RESULT 7	
AQ265389/c	577 bp DNA GSS 27-OCT-1998
LOCUS	CITBI-21-2509010.TF CITBI-EI Homo sapiens genomic clone 2509010,
DEFINITION	DNA sequence.
ACCESSION	AQ265389
VERSION	AQ265389.1 GI:3793589
KEYWORDS	GSS.
SOURCE	human.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 577)	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building	Unpublished (1998)	
	Other_GSSs: C17B1-E1-2509010.TR	Contact: Mark Adams	Department of Eukaryotic Genomics	
	9712 Medical Center Dr., Rockville, MD 20850, USA	Tel: 301 838 0200		
	Fax: 301 838 0208	Email: mdadams@ftrg.org		
	Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.ftrg.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21			
	Class: BAC ends.			
FEATURES	source	location/Qualifiers		
		1..577		
		/organism="Homo sapiens"		
		/db_xref="taxon:9606"		
		/clone="2509010"		
		/clone_11b="C17B1-E1"		
		/sex="male"		
		/cell_type="sperm"		
		/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"		
BASE COUNT	167 a	127 c	137 g	146 t
ORIGIN				
Query Match	3.3%	Score 177.4;	DB 91;	Length 577;
Best Local Similarity	75.1%;	Pred. No. 3.2e-21;		
Matches 238;	Conservative 0;	Mismatches 71;	Indels 8;	Gaps 1;
QY	1321	acctagctcatgtaaacactcgtccctccagtgtaagcaattctcgtctacagcccc	1380	
DB	368	ATCTGGGCTCATGTGCAACCTCGCTCCACAGGTTCAATGATCTCTGCTCCACACCTTC	309	
QY	1381	cgcgtacgtctgtaacacagggc-----gcacgcccgtcaatttttgtattgttgta	1432	
DB	308	CGAGTATCTAGAGACTACAGGCAACCCGCCACCAAGCCTGGCTAATTTTGGTATTTTATA	249	
QY	1433	ggagatggtttcacacataatagcccggtctggtcttgaactctcgaacctcagtgata	1492	
DB	248	GAGACGGGGTTTCACCAATGTTGTGTGAGCGTGCTTTGAATCTGACCTCAGGCGATCCA	189	
QY	1493	cccactcagcctctctaaagtgtctggtattaaagcatgagtacacggcccgccgacaa	1552	
DB	188	CCCGCTTGCGCTCCCAAGTGTGGGATTAAGGCATGAGCACTGACCCAGCCAGA	129	
QY	1553	gtcagtggttaataagaaactcgaatgtgttactaaaccaacagggaacagacaaa	1612	
DB	128	GATTAATTTTGTTAATCTAGACTGGAGTCACTGAGACAGCTCTCAGGCAAAAGGAGAA	69	
QY	1613	agctgtgataaatttcag	1629	
DB	68	ACTAATACTGATGAG	52	
RESULT	8			
LOCUS	AI583291	548 bp	mRNA	EST
DEFINITION	tt56g02.x1 NC1 CGAP_HSC4 homo sapiens cDNA clone IMAGE:2244818	3'		
ACCESSION	AI583291			

VERSION	AT583291.1	GI:456198
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 548)	
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Kitzman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILWU at: www-bio.lnl.gov/bbrp/image/image.html Insert Length: 664 Std Error: 0.00 Seq primer: -400P from Glbco PolyA-No.	

FEATURES	Location/Qualifiers
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/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2244818"
 /clone_1ib="NCI_CGAP_HSC4"
 /tissue_type="CD34+", CD38- from normal bone marrow donor"
 /lab_host="DH10B"
 /note="Organ: bone marrow; Vector: pAMP1; mRNA made from lymphoid tissue; cDNA made by oligo-dT priming. gel, directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA library Preparation: David B. Kitzman, Ph.D. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383"

Query Match	3.3%	Score 177.2	DB 11	Length 548
Best Local Similarity	78.8%	Pred. No. 3.5e-21		
Matches 227	Conservative	0	Mismatches 53	Indels 8
			Gaps 1	
QY 1277	gtgaagggtgaagggtctgtgtcttacaaccatactgtatgtcttacaacctagctcaatgca	1336		
DB 546	GAGGAGNCTTTATCTGTCTCTCAGGCTGAGTGCAGTGCATGATCTTGCTCACTGCA	487		
QY 1337	acctctgcctcccaaggttcaagaacattctctctgtctcaagctcccgctagcttgagacta	1396		
DB 486	ACCTCGCCTCACAGGTTCAAGCAATTCCTCCGCCACCTCTCGAGCAGCTGAGACTA	427		
QY 1397	caggcg-----caggccggcgcaattttgttatgttagtaagaatggggtttacc	1448		
DB 426	CAGGGCCCCGCCACACACGCTGGCTAATTTTGTATTTTGTAGTAGAGATGGGATTTCAC	367		
QY 1449	atatatgaccggctgtgtcttgaacttctgaacttcaagttatcatcacccacctcagctcct	1508		
DB 366	ATGTTGGCCAGGCTGTGTGGAATCCTCACTCAAGTGATCACCACCACTTGTCCTCC	307		
QY 1509	aaatgctctggaattacagcatgagtcaaccggcccgcccgccaaggttca	1556		
DB 306	AAAGTCTGTGGATTACAGCATGAGCCACCGTCCAGCCACAGATTTA	259		

RESULT	9				
AO199435/c					
locus					
AO199435		434 bp	DNA	GSS	20-APR-1999

DEFINITION	RPc111-58F5.TJ RPc11 Homo sapiens genomic clone RPc11-58F5, DNA sequence.
ACCESSION	AQ19435
VERSION	AO19435.1 GI:3611634
KEYWORDS	GSS.
SOURCE	human.

ORGANISM	REFERENCE
Homo sapiens	Adams M.D., Rounsley S.D., Zhao S., Bass S., Linher K., Golden K., Berry K., Granger D., Suh E., Mible C., de Jong P. and Venter J.C.
Eukaryota; Metazoa	Unpublished (1998)
Mammalia; Eutheria	Other_GSSS: RPI11-56F5.1TK
Primates; Catarrhini; Hominoidea; Homo.	
1 (bases 1 to 434)	
Use of human BAC End Sequences for Sequence Ready Map Building	
Unpublished (1998)	
Other_GSSS: RPI11-56F5.1TK	

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPEC1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACpac Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .434

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/clone_1b="RPC1-11"
/sex="Male"
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/notes="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"

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	Best Local	Similarity	77.4%	Pred	No.	4.5e-21:				
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Qy	1292	tggtcttacacctaactgtagtctctacacctaagctactgtcaacctctgctccag	1351							
Db	427	ttctactcaggtgagtgacatggacacatcttggtctctctgcacacctctctctctg	368							
Qy	1352	gttcaagaacattctctctgtctcagacctccgcgtagtctggaataagc-----gc	1403							
Db	367	gtttcaagcattctctctgtctcagcctcccaagttacagcaccggccacac	308							
Qy	1404	acgcccgcgtaaatttttgtaattgtaagagacgggggtttcaacatatagccgcgctg	1463							
Db	307	atgcccgctaatatttttgatttttttgatgacacatggcggtttacatagtgtgcccctgac	248							
Qy	1464	gtcttaaacctctgacctaaagtgtatcacacccacactcaagccctcctaaagtgtggat	1523							
Db	247	gtctgcaaatccggacctagctgactgactcaccctgccttggtgcccctcctgaaatgc	188							
Qy	1524	caggcatgtagtaccgcgcgcggcccaagggtctagtgcttaataaggataaacttgaa	1580							
Db	187	caggctgtgtgtagtaccctgaccacgcagagtgatgggtttttatccaggaaagacttgaa	131							

RESULT	10		
AM979191			
LOCUS	AM979191	591 bp	EST
DEFINITION	EC3391301 MAGE resequences, MACP Homo sapiens CDNA, mRNA sequence		

ORGANISM Homo sapiens
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.

REFERENCE 1 (bases 1 to 551)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Donald, M.F., Chiapelli, B., Chisnoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellendberg, K., Soares, M.B., Tan, F., Tillery-Weg, J., Trevaakis, E., Underwood, R., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (4), 807-828 (1996)

TITLE JOURNAL MEDLINE
 97044478

COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel.: 314 286 1800
 Fax: 314 286 1810
 Email: estevatson.wustl.edu
 Insert Size: 760
 High quality sequence strops: 380 Source: IMAGE Consortium, LINT This clone is available royalty-free through LNC; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 760 Std Error: 0.00
 Seq primer: -21m3
 High quality sequence stop: 380.
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 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: liver; Vector: plasmid; SK: Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTATTTTATTTT 3'"

BASE COUNT 119 a 134 c 127 g 163 t 8 others

ORIGIN

Query Match 3.3% Score 176; DB 39; Length 551;
 Best Local Similarity 80.7%; Pred. No. 5.6e-21;
 Matches 221; Conservative 0; Mismatches 45; Indels 8; Gaps 1;

OY 1321 accgtagctcaactgcgaacctctgctcccaaggttaagaacatctccgtctcaagctcc 1380
 DB 47 ATCTTGCGCTCATCTGGACCTCTGCCTCCACGATTCAAGGATTCTCGCCACACCTCC 106

OY 1381 cgcgtagctcgtgacacagggcg-----cagcgccggtcaatttggatgttaagta 1432
 DB 107 TGAGTAGCCAGGATTACAGGTGCCGCCACCCACACCACTTAATTTTGTATTTTAA 166

OY 1433 gagaatgggtttcacacatatatgacccggctgtgtcttgaaactcctgaactcaagtgatcca 1492
 DB 167 GAGATGGGGTTTCACTATGTTGGCCAGGCTATCTTTTACTCTTACCTCAGGTGATCA 226

OY 1493 cccaccacagcctcctctaaagtgtcgtggaattacagacatgagtcaccggtcccgccaaag 1552
 DB 227 CCCGCTCAGCTCCCAAGTGTCTGGGATTACAGGCAATGAGTACCAGCCCTGCGCTTTC 286

OY 1553 gtccagtgtttaataagaaataaactcgaatggtt 1586
 DB 287 CTGACTTTTAACTGATCAACATTCTAAGTGTAT 320

LOCUS	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
LOCUS	AO283440	589 bp	DNA	GSS	27-APR-1999					
DEFINITION	RPc111-7965.TJ	RPc1-11	Homo sapiens	genomic clone	RPc1-11-7965, DNA					
SEQUENCE	1 (bases 1 to 589)									
ADDITIONAL	AO283440									
KEYWORDS	AO283440.1	GI:3908257								
SOURCE	human.									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Mable,C., de Jong,P. and Venter,J.C.									
TITLE	Use of human BAC End sequences for Sequence-Ready Map Building									
JOURNAL	Unpublished (1998)									
COMMENT	Other_GSSs: RPc111-7965.TJ									
	Contact: Mark Adams									
	Department of Eukaryotic Genomics									
	The Institute for Genomic Research									
	9712 Medical Center Dr., Rockville, MD 20850, USA									
	Tel: 301 838 0200									
	Fax: 301 838 0208									
	Email: maddams@tigr.org									
	Clones are derived from the human BAC library RPc1-11. For BAC									
	library availability, please contact Pieter de Jong									
	(pieter@tigr.org, med.buffalo.edu). Clones may be purchased from									
	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from									
	Research Genetics (info@resgen.com). BAC end search page:									
	http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html									
	Seq primer: SP6									
	Class: BAC ends.									
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Best Local Similarity	75.7%;	Pred. No. 6e-21;								
Matches 234;	Conservative 0;	Mismatches 67;	Indels 8;	Gaps 1;						
OY	1280	agggtgagaggtctgtgtcttacactactctttagcttacaacttgagactctgagctactgcaacc	1339							
DB	105	AGAGCTCTTGCTCTTGCGCCAGCGTGAAGTACAGTGTGCATGTGCACCTGACCTGCAACC	164							
OY	1340	tctgctctccagaggttcagagaacttctctgtcttcagagctcccgcgtagctggagactacag	1399							
DB	165	TCTGACTCTCTGGGTTCAAGCAATTCTCTGTCTTACGCCCCCGAGTACCTGGGATTACAG	224							
OY	1400	gcg-----cacgccccgactaaattttgtatgtgttagtagagatgaggtttcaaccata	1451							
DB	225	GTCCTGCGCACCATGCTCAGCAATTTTGTATTTTGTAGACACAGATGGGGTTTACACATA	284							
OY	1452	ttagccgagctgtgtcttctgaaactctgacctcagtgatgataccaccaccctcagctctctaa	1511							
DB	285	TTGGTCAGAGCTGTGTTGGAACATCTCGACCTCATGTGATGCACCCGTCACCTGCCCAA	344							
OY	1512	gtgcgaggaatacagagcattgagttacccgccccgagccagaggtctgatttaataagga	1571							
DB	345	GTGCTGGGATTACAGCGCTGAGCCACCTGCTGCTGCTCCAGGGGTGATGTTTATTAGGA	404							
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DB	405	TAACTTGCA 413								

DB 65 CTTGCTGCTTTTGTA 48

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Job time: 13973 sec